

ABSTRACT OF THE DISCLOSURE

Methods of creating libraries of biological polymers are provided. The construction of a library employs a probability matrix for a reference sequence, and a constraint vector for which is applied to the probability matrix to produce a substitution scheme. The substitution scheme is then used to generate a library comprising substitutions recommended by the substitution scheme. The library members, or host cells comprising and/or expressing them, can be screened for desired changes in a property of interest in the biological polymers in the library.